

FIGURE 1

1  
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG  
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu  
46  
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTTCCTCCTGCC  
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla  
91  
GGGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG  
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu  
136  
CGGAGCGCGCGCGGGCGGGGGCTGCGCAGCTGGCGCACCTG  
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu  
181  
CACGGCATCTGCGCCGCCGCGCAGCTCTATTGCCGCACCGGCTTC  
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe  
226  
CACCTGCAGATCCTGCCCGACGGCAGCGTGCAGGGCACCCGGCAG  
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln  
271  
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG  
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal  
316  
GGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA  
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly  
361  
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC  
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer  
406  
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC  
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr  
451  
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT  
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr  
496  
TTTGTGGCACTTAACAAAGACGGAACCTCAAGAGATGGCGCCAGG  
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg  
541  
TCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCACTG  
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal  
586  
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC  
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr  
631  
ACT  
Thr

Query: 170 TGGCGCACCTGCACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229  
 ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCACT 61

Query: 230 TGCAGATCCTGCCCACGGCAGCGTGCAGGGCAGCCGGCAGGACCACAGCCTCTTCGGTA 289  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 62 TAGAAATCTTCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

Query: 290 TCTTGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC 181

Query: 350 TCTATCTTGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCCGAAT 409  
 |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query: 410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTTCATCTAACATATATA 469  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 242 GTGTATTTCAGAGAACAGTTTCGAAGAAAACCTGGTATAATACGTACTCGTCAAACCTATATA 301

Query: 470 AACATGGAGACACTGGCCGAGGTATTTTGTGGCACTTAACAAAGACGGAACCTCCAAGAG 529  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 302 AGCACGTGGACACTTGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query: 530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589  
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query: 590 CAGA 593  
 | | |  
 Sbjct: 422 CCGA 425

**FIGURE 3**

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

**A.**

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
Identities = 288/289 (99%), Positives = 288/289 (99%),  
Strand = Minus / Plus

```
Query: 289 TACCGAAGAGGCTGTGGTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
      |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query: 229 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
      |||
Sbjct: 15987 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCG -CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query: 169 GCTGCGCAGCCCCCGCCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 110
      |||
Sbjct: 16046 GCTGCGCAGCCCCCGCCCCGCCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 16105

Query: 109 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCACCTGCTGGCCCA 50
      |||
Sbjct: 16106 GCAGCGGCGGCCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCACCTGCTGGCCCA 16165

Query: 49 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 1
      |||
Sbjct: 16166 AGCCCTCCAGGCCGCCAGAAAGCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

**B.**

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
Identities = 250/255 (98%), Positives = 250/255 (98%),  
Strand = Minus / Plus

```
Query: 633 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 574
      |||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTACAATTCTGGAACCTTTTCTGGATCCACTGGTCTAGG 7316

Query: 573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 514
      |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGACCTGGCGCCATCTCTTGAGTTCCGTC 7376

Query: 513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
      |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query: 453 ATAGGTGTTATACCAAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 394
      |||
Sbjct: 7437 ATAGGTGTTATACCAAGTTCTCTTCAAACCTGCTCCCTAAAGATGCATTGGAAGTAAGTTT 7496
```

# FIGURE 3 (cont.)

Query: 393 CTC-TGATCCATAGA 380  
 ||| ||| | |||  
 Sbjct: 7497 CTCCTGAAAGAGAGA 7511

## C.

Score = 530 (79.5 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126  
 Identities = 106/106 (100%), Positives = 106/106 (100%),  
 Strand = Minus / Plus

Query: 391 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 332  
 |||||  
 Sbjct: 9837 CTGATCCATAGAGTTCTCCTTTGTCATTTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query: 331 TAATACTGACCAGTCCCACTGCCCACTGATGAATTCCAAGATACC 286  
 |||||  
 Sbjct: 9897 TAATACTGACCAGTCCCACTGCCCACTGATGAATTCCAAGATACC 9942

# FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371\_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130\_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364\_FGF9\_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L N D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T F L G G Y D A L G - Q V G S H F L L P P A K D S P L L F N D P L A Q S E R L S R - S L A P - - S D L S H
M A P L A E V G G F L G G L G G L G Q Q V G S H F L L P P A G E R P P L L G E R R S A A E R S A R - G G P G A A Q L A H

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HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S V A G L V S I R G V D S G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F I S V A V G L V S I R G V D S G L Y L

```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y Y F V A L N K D G T P R D G T
G M N D K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D T G R R Y Y F V A L N K D G T P R D G A

```

HUMAN FGF-9

RAT FGF-9

MOUSE FGF-9

XENOPUS XFGF-CX

FGF-CX

```

R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P D K V P E L Y K D L M G Y S
R S K R H Q K F T H F L P R P V D P D K V P E L Y K D L L M Y T

```

FIGURE 5

FGF-CX	MAPLAEVGGFL EGLEGLQAVESHFLPPA GERPPILLGERSAERSAR - EGP GAAQLAH	59
XFGF-2U	MAPLADVGTFL EGYDALG - QVESHFLPPAKDSFLL ENDPILAQSRLSE - SAP - - SDLSH	56
FGF-9	MAPLGEVGNMFVQDAVP - - FENVPVLP - - VDSFVLLSDHLGQSEAGGLPRPPAVTEL DH	56
FGF-16	- - - MAEVGGVFASLDWDLHGFS SLGNVPLADSPGFLNERLGQIEGKLQRES P - - IDFAH	55
FGF-CX	LHGILRRRQLYCRTGFHLQILFDGSVQGTRODHS LFGILEFISVAVGLVSIRGVD SGLYL	119
XFGF-20	LQGI LRRRQLYCRTGFHLQILFDGNVQGTRODHSRFGILEFISVAGLVSIRGVD TGLYL	116
FGF-9	LKGILRRRQLYCRTGFHLEIFENGTQQGTRKDHRSRFGILEFISVAVGLVSIRGVD SGLYL	116
FGF-16	LKGILRRRQLYCRTGFHLEIFENGTVHGTRHDHSRFGILEFISVAVGL VSIRGVD SGLYL	115
FGF-CX	GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNLYKHGDTGRRYFVALNKDGTPRDGA	179
XFGF-20	GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNLYKHGDSGRRYFVALNKDGTPRDGT	176
FGF-9	GMNEKGELYGSEKLTQECVREQFEENWYNTYSSNLYKHVD TGRYYVVALNKDGTPREGT	176
FGF-16	GMNERGELYGSKKLTRECVREQFEENWYNTYASTLYKHS DSE RQVYVVALNKDGS PREGY	175
FGF-CX	RSKRHQKFTTHFLPRP VDPERWPELYKDL L MVT	211
XFGF-2U	RAKRHQKFTTHFLPRP VDPEKVP ELYKDL MGV S	208
FGF-9	RTKRHQKFTTHFLPRP VDPDKVP ELYKDL L S QS	208
FGF-16	RTKRHQKFTTHFLPRP VDPSK LFSMSRDL FHR	207

# FIGURE 6

ptnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

Query:	1	MAPLA	EVGGFLG	GLGQQV	GSHFL	PPAGER	PPLLG	ERRSAA	ERSARG	-GPGAA	QLAH	59				
Sbjct:	1	MAPL	GEVGN	YFGVQ	DAV--	PFGN	VPVLP	V--DSP	VLLSD	HLGQ	SEAGGL	PRGPA	VTDL	DH	56	
Query:	60	LHGIL	RRRL	QLYCR	TGFHL	QILL	PDGS	VQGT	RQDHS	LFGIL	EFIS	VAVGL	VSIR	GVDS	GLYL	119
Sbjct:	57	LKGIL	RRRL	QLYCR	TGFHL	EIFPN	GTIQ	GTRK	DHSR	FGIL	EFIS	AVGL	VSIR	GVDS	GLYL	116
Query:	120	GMNDK	GELYG	SEKLT	SECIF	REQF	EENW	YNTY	SSNI	YKHG	DTGRR	YFVA	LNKD	GT	PRDGA	179
Sbjct:	117	GMNEK	GELYG	SEKLT	QECV	FREQ	FEEW	YNTY	SSNL	YKHV	DTGRR	YFVA	LNKD	GT	PREGT	176
Query:	180	RSKR	HQKFT	HLPR	PVDP	PERV	PELY	KDIL	208							
Sbjct:	177	RTKR	HQKFT	HLPR	PVDP	PD	KVPE	LYKDIL	205							

# FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76  
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```

Query:      1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
            |||| ||| + | + + + + || + || + + | || || |
Sbjct:      1 MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLNDHLGQSEAGGLPRGPAVTDLDH 56

Query:     60 LHGILRRRQLYCRTGTFHLQILPDGSVQGTQDHSLEFISVAVGLVSIRGVDSGLYL 119
            | |||| |||| |||| ||| + || + |||| |||| + |||| |||| |||| |||
Sbjct:     57 LKGILRRRQLYCRTGTFHLEIFPNGTIQGTQKHSRFGILEFISIAVGLVSIRGVDSGLYL 116

Query:     120 GMNDKGELYGSEKLTSECFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
            ||| + |||| |||| ||| + |||| |||| |||| |||| + |||| + |||| |||| +
Sbjct:     117 GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYVVALNKDGTREGT 176

Query:     180 RSKRHQKFTHFLPRPVDPERVPELYKDIL 208
            | + |||| |||| |||| ||| + |||| |||| ||| +
Sbjct:     177 RTKRHQKFTHFLPRPVDPKVPELYKDIL 205
    
```



Length = 208

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76  
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```

Query:      1  MAPLAENVGGFLGGLEGLGQQVGSFHLLPPAGERPPLLGERRSAAERSARG-GPGAAQLAH  59
          ||||| + | + + + | + | + | + | + | + | + | + | + | + |
Sbjct:      1  MAPLGEVGSYFGVQDAV--PFGNVFVLPV--DSPVLLSDHLGQSEAGGLPRGPVAVTDLDH  56

Query:     60  LHGILRRRQLYCRTGFHLQLPDGGSVQGTQRQDHSLSFGILEFISVAVGLVSIQVDSGLYL  119
          | ||||| ||||| ||||| + | + + ||||| + ||||| ||||| ||||| |||||
Sbjct:     57  LKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIQVDSGLYL  116

Query:     120  GMNDKGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA  179
          ||| + ||||| ||||| + ||||| ||||| ||||| ||||| ||||| ||||| + |
Sbjct:     117  GMNEKGELYGSEKLTQECVREQFEENWNTYSSNLKYHVDTCRRYYVALNKDGTPREGT  176

Query:     180  RSKRHQKFTHFLPRPVDPERVPELYKDLL  208
          | + ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| + |
Sbjct:     177  RTKRHQKFTHFLPRPVDPDVKPELYKDLL  205

```

# FIGURE 9

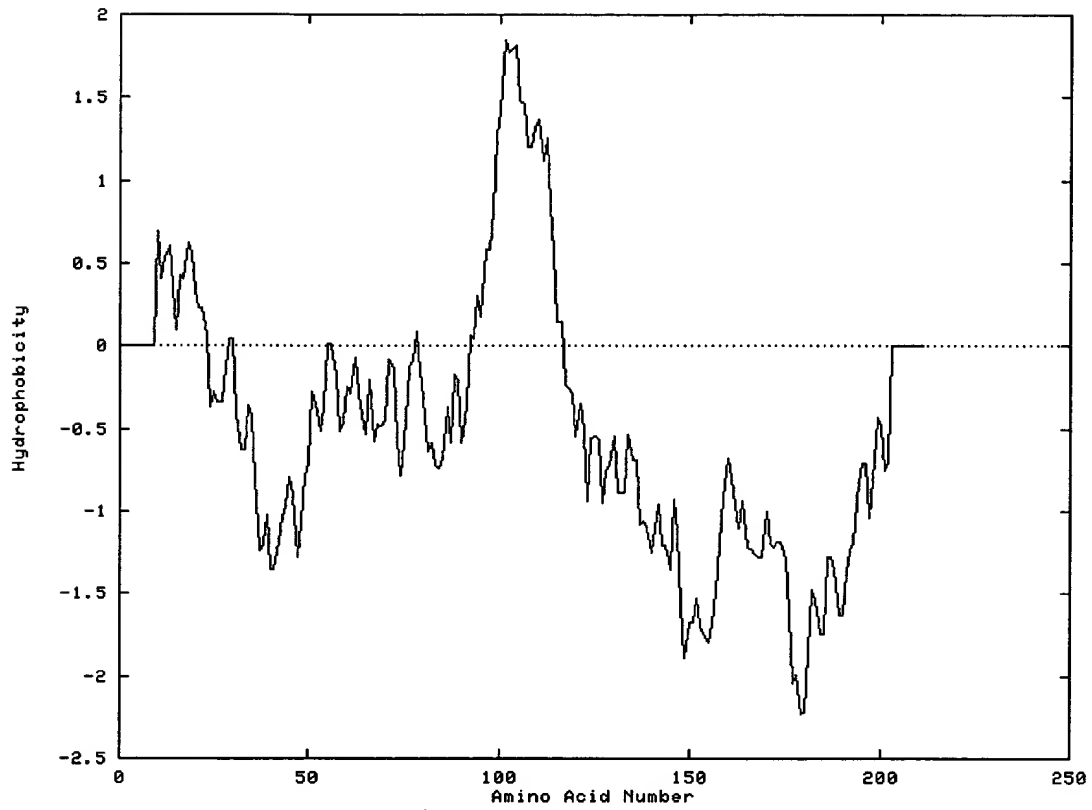
FGF-CX Query Length = 211  
XFGF-CX Sbjct Length = 208

## Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90  
Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

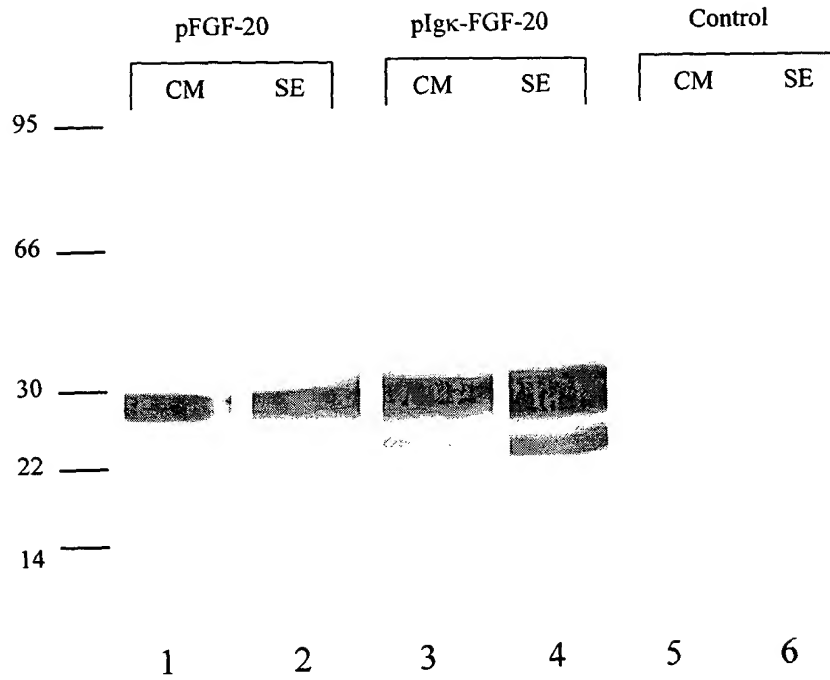
Query:	1	MAPLAEVGGFLGGLGQQVGS	60
		+        +	
Sbjct:	1	MAPLADVGTFLGGYDALGQ-VGSHFLLPPAKDSPILLFNDPLAQSERLSRSAP--SDLSHL	57
Query:	61	HGILRRRQLYCRTGTFHLQILPDG	120
		+        +	
Sbjct:	58	QGILRRRQLYCRTGTFHLQILPDG	117
Query:	121	MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGT	180
		+        +	
Sbjct:	118	MNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDSGRRYFVALNKDGT	177
Query:	181	SKRHQKFTHTFLPRPVPDP	211
		+   +        +	
Sbjct:	178	AKRHQKFTHTFLPRPVPDP	208

FIGURE 10

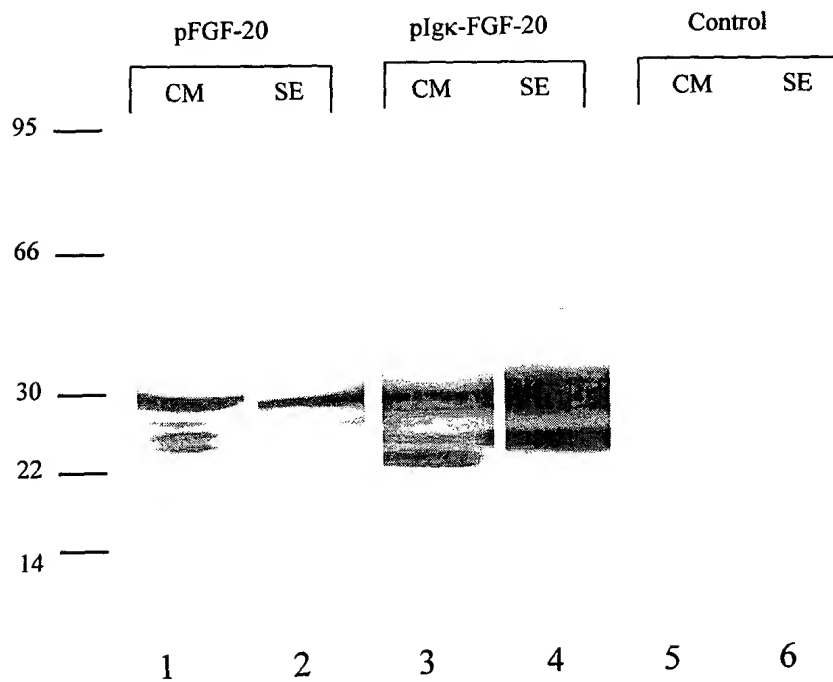


**FIGURE 11**

**Panel A**



**Panel B**



**FIGURE 12.**

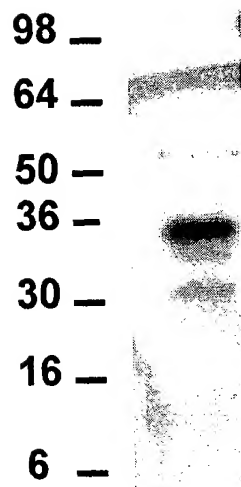


Figure 13.

Exon 1  
...AGACAGTGAGAGCTTCCCTGCCATTTTCAGTGTCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGGCCTTAAC  
TTTTGGGCTCGTTTTGCTATAATTTTCTCTATCCACCTCCATCCACCCCAACACTCTTTACTGGGGGGTCTTTTT  
GTGTTCCGGATCTCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGCGGGCTTGAGGGCTTGGGCCAGCA  
1 M A P L A E V G G F L G G L E G L G Q Q  
GGTGGTTTCGCATTTCTGTTCCTCCTGCCGGGAGCGCGCGCTGTGGCGAGCGCAGGAGCGCGGAGCGGA  
21 V G S H F L L P P A G E R P P L L G E R R S A A E R S  
GCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTGCACGGCATCTGCGCGCGCGGAGCTCTATTGCCGCACC  
48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T  
GGCTTCCACCTGCAGATCCTGCCCGACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTATCTTGGAAAT  
74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F  
<-|-> Exon 2  
CATCAGTGTGGCAGTGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGAAATGAATGACAAGGAGAAC  
101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L  
<-|-> Exon 3  
TCTATGGATCAGAGAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCT  
128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S  
AACATATATAAACATGGAGACACTGGCCCGCAGGTATTTTGTGGCACTTAACAAAGACCGAACTCCAAGAGATGGCGCCAG  
154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R  
GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCCAGAATTGTACAAGGACC  
181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L  
TACTGATGTACACTTGA...  
208 L M Y T

Figure 14.

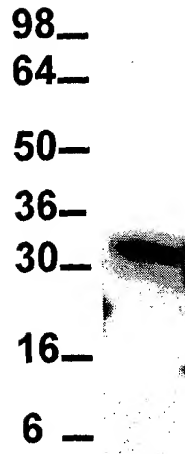


Figure 15, Panel A.

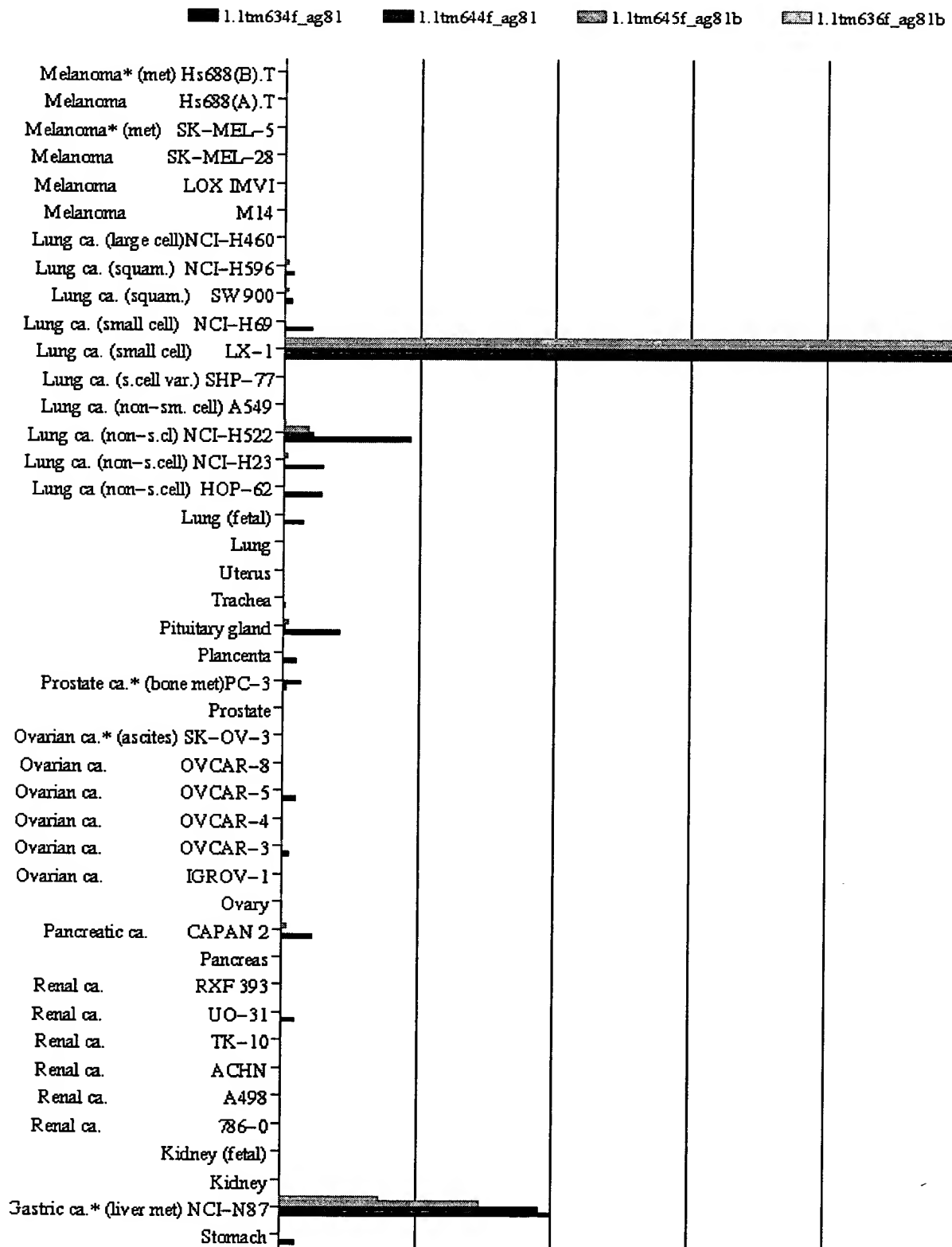




Figure 15, Panel B.

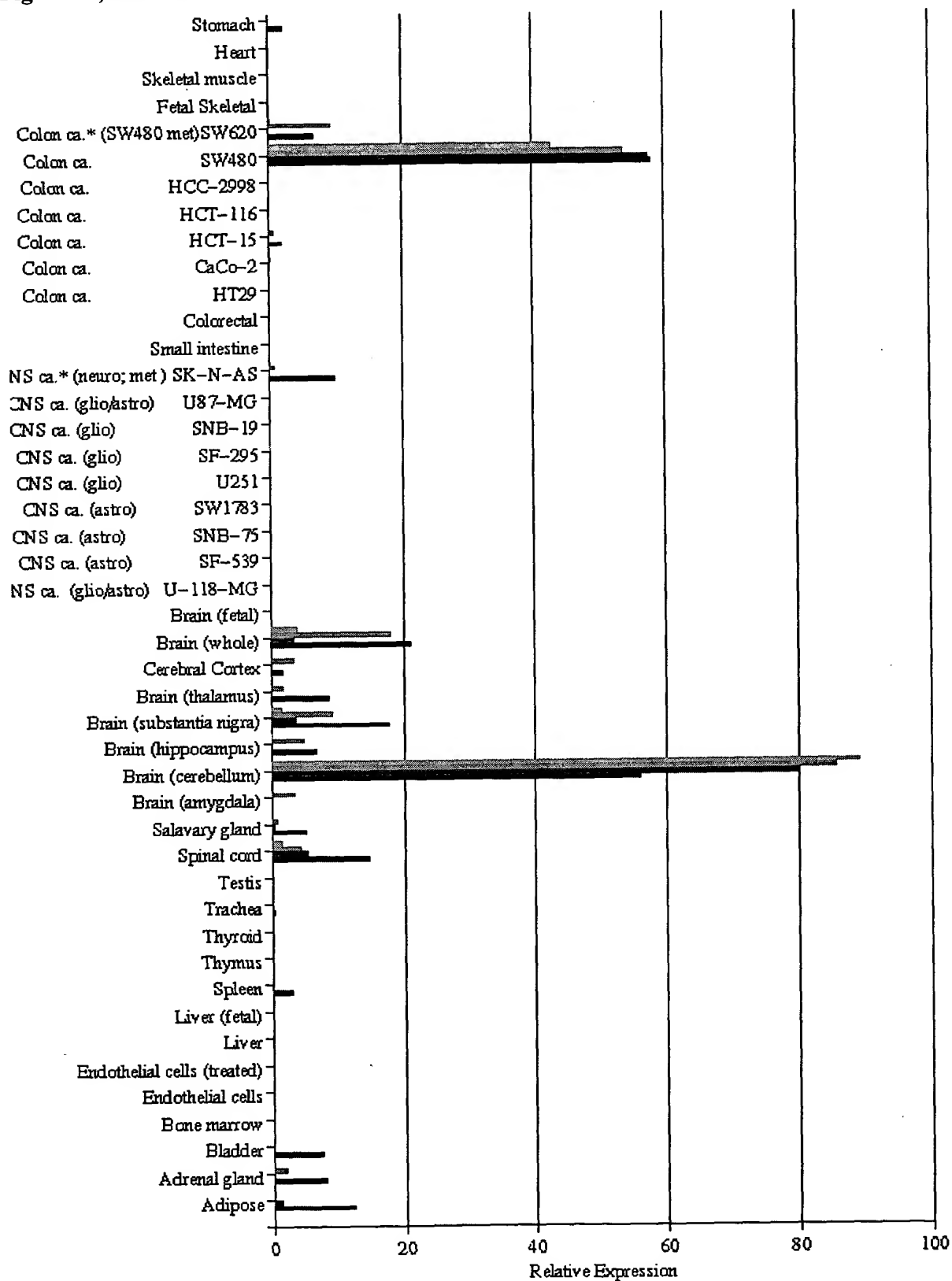


Figure 15, Panel C.

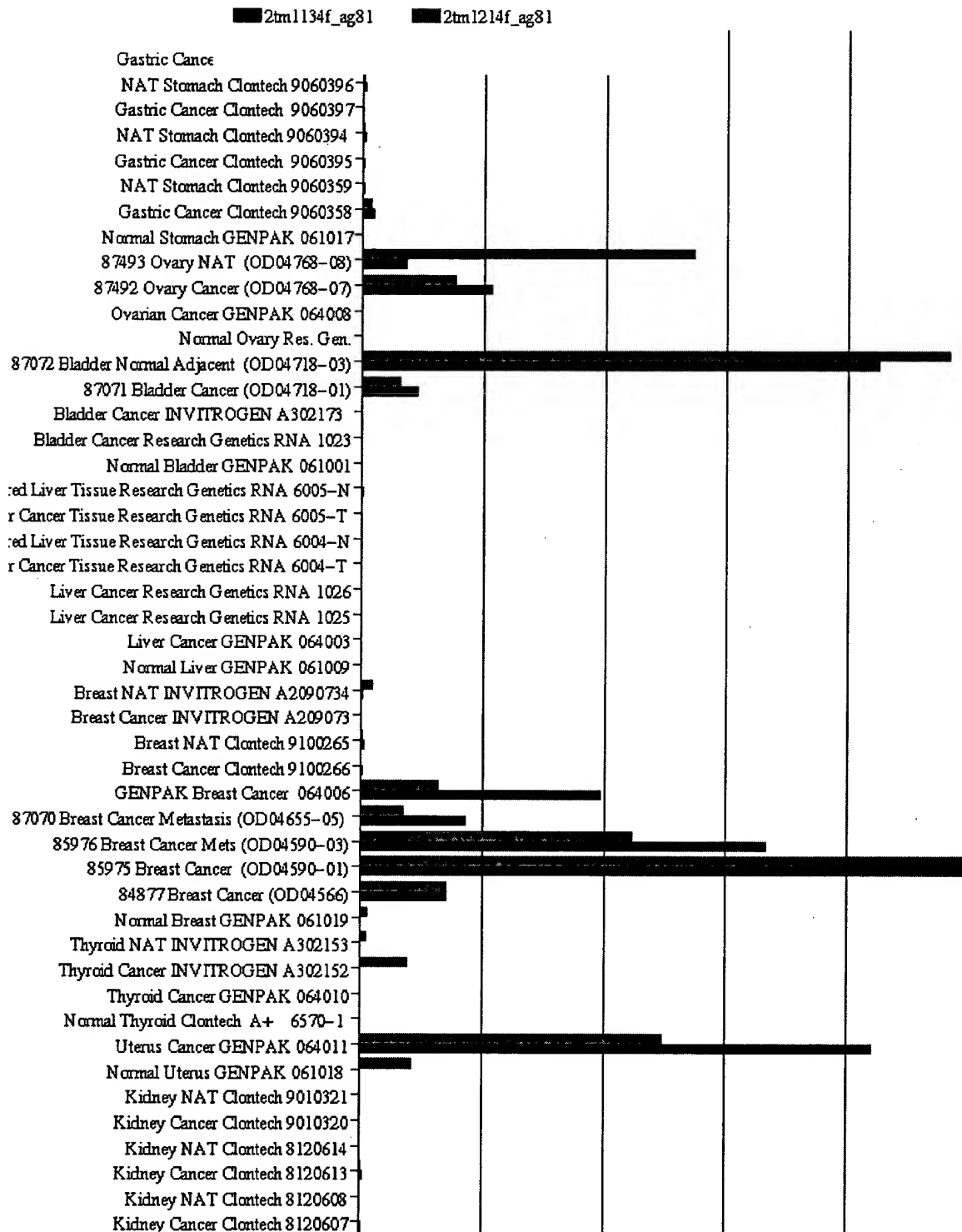


Figure 15, Panel D.

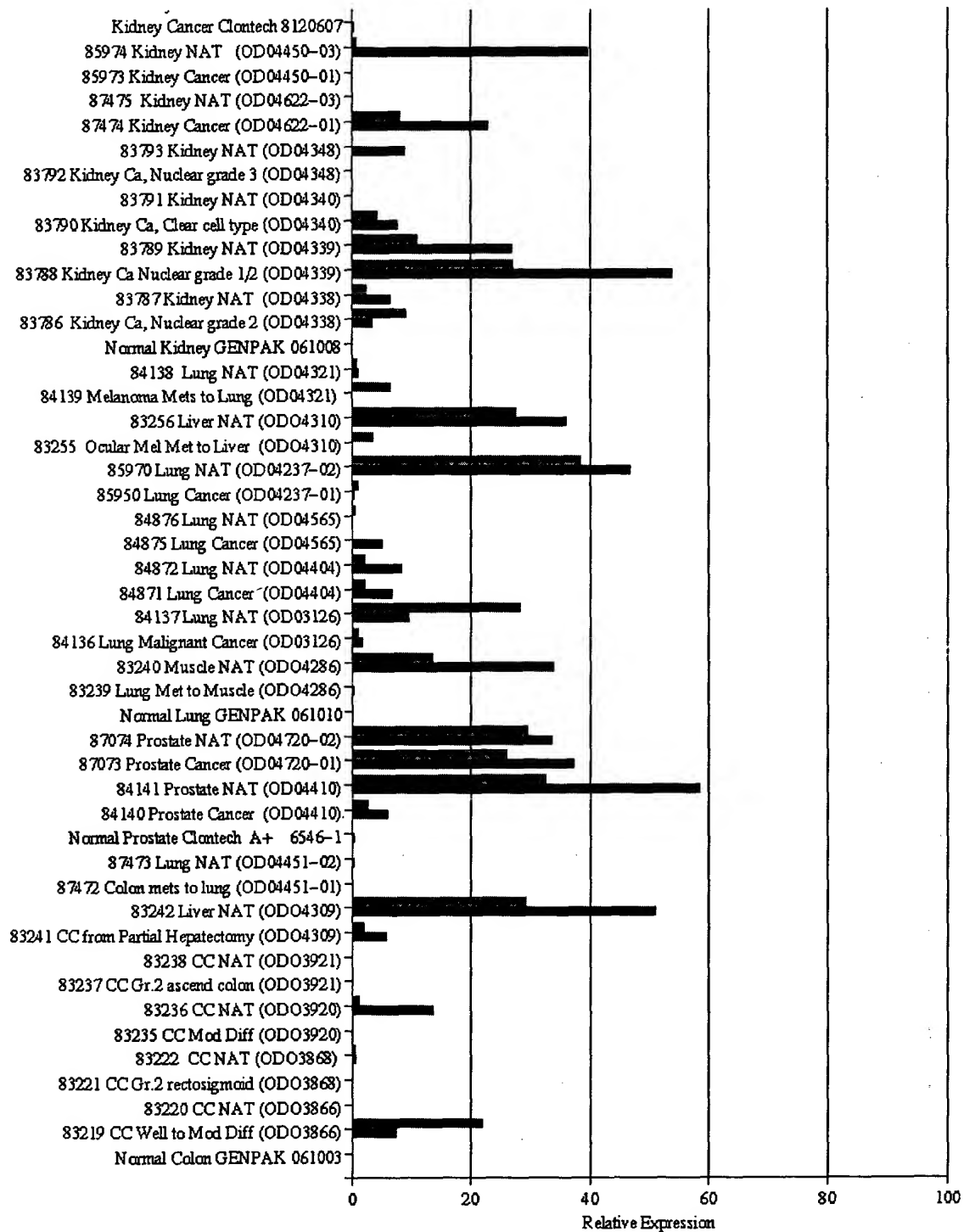


FIGURE 16.

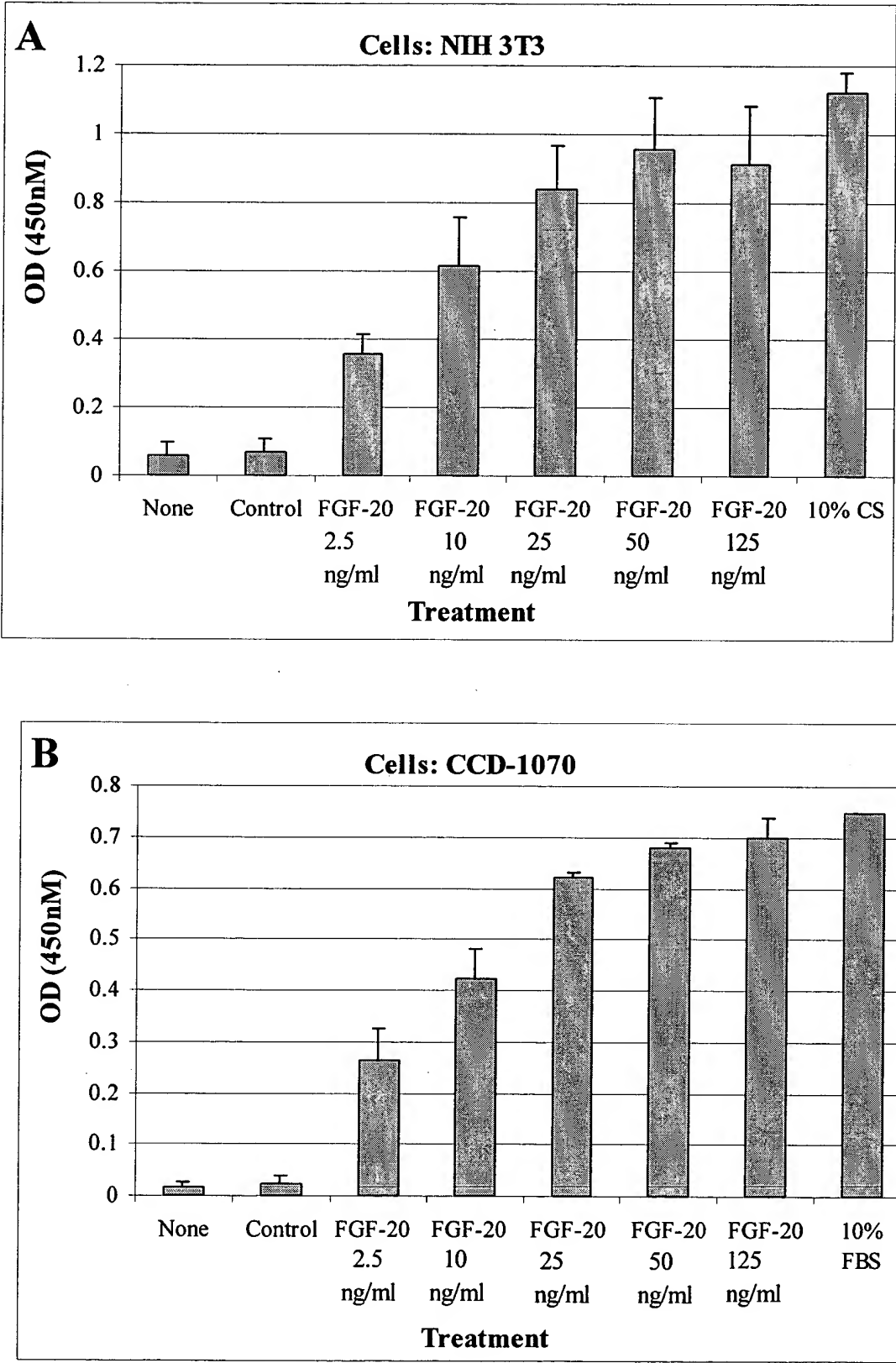


FIGURE 16 (continued).

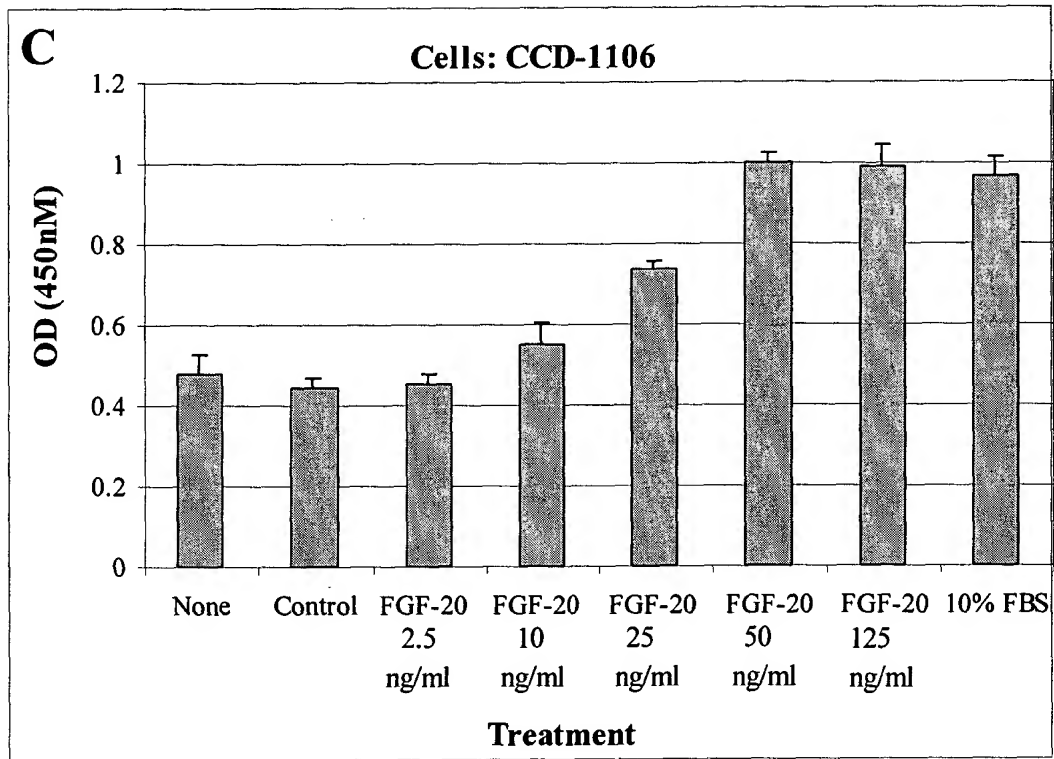


FIGURE 17.

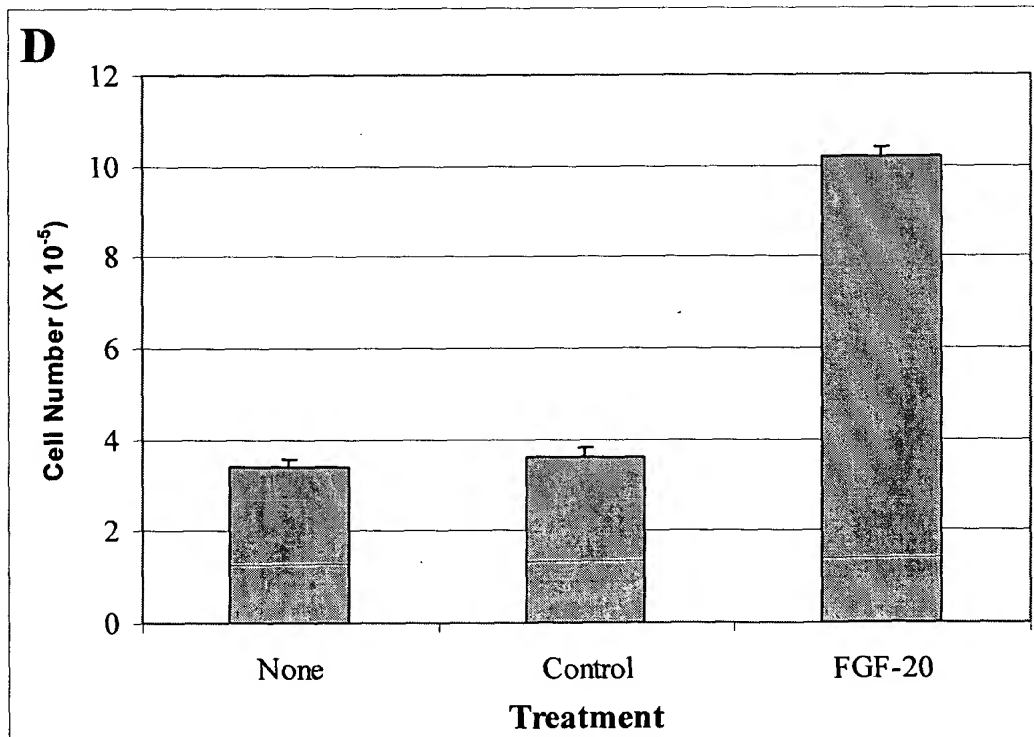


FIGURE 18.

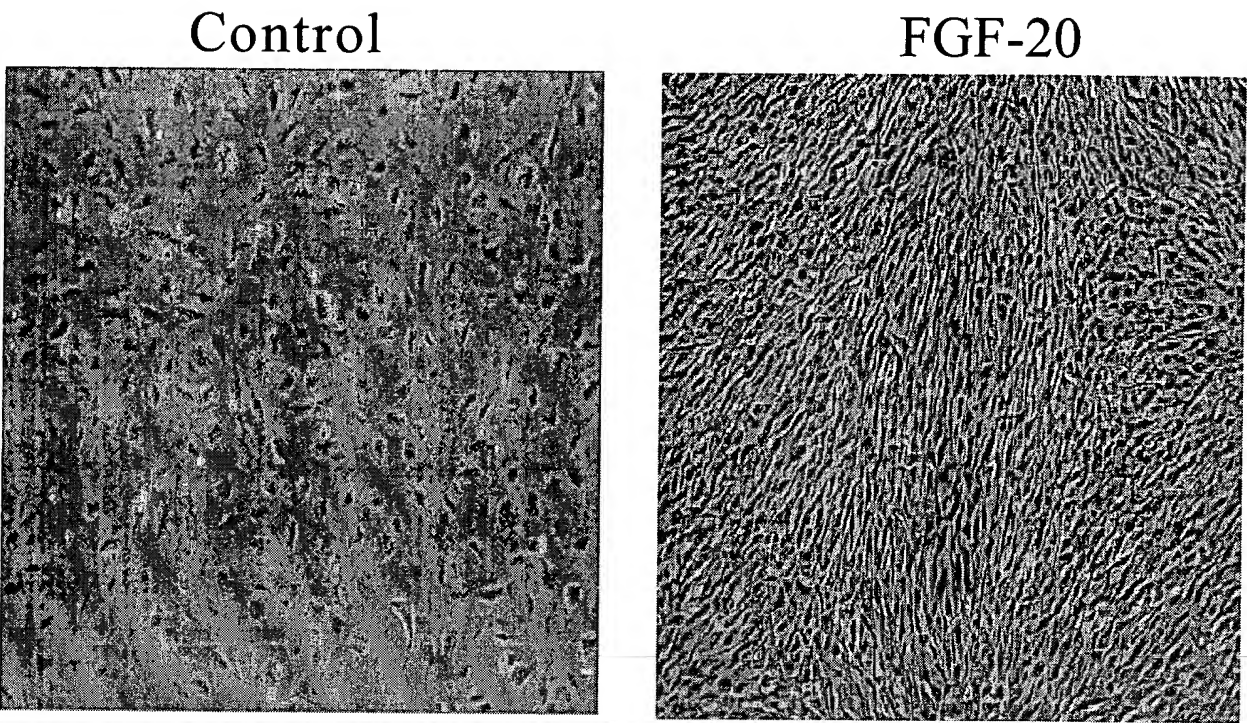
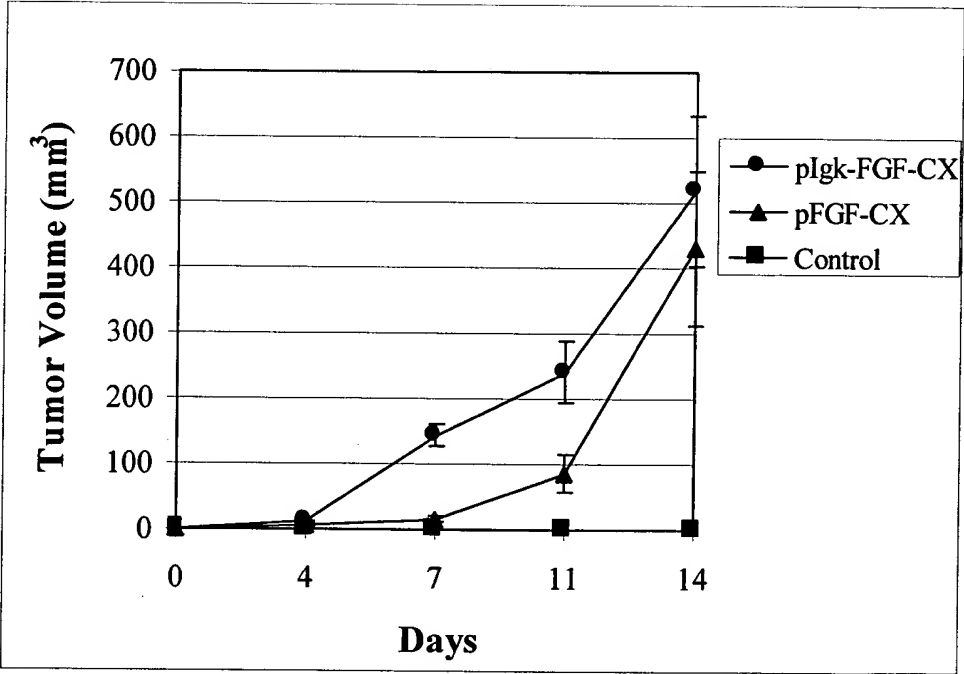


FIGURE 19.



**FIGURE 20.**

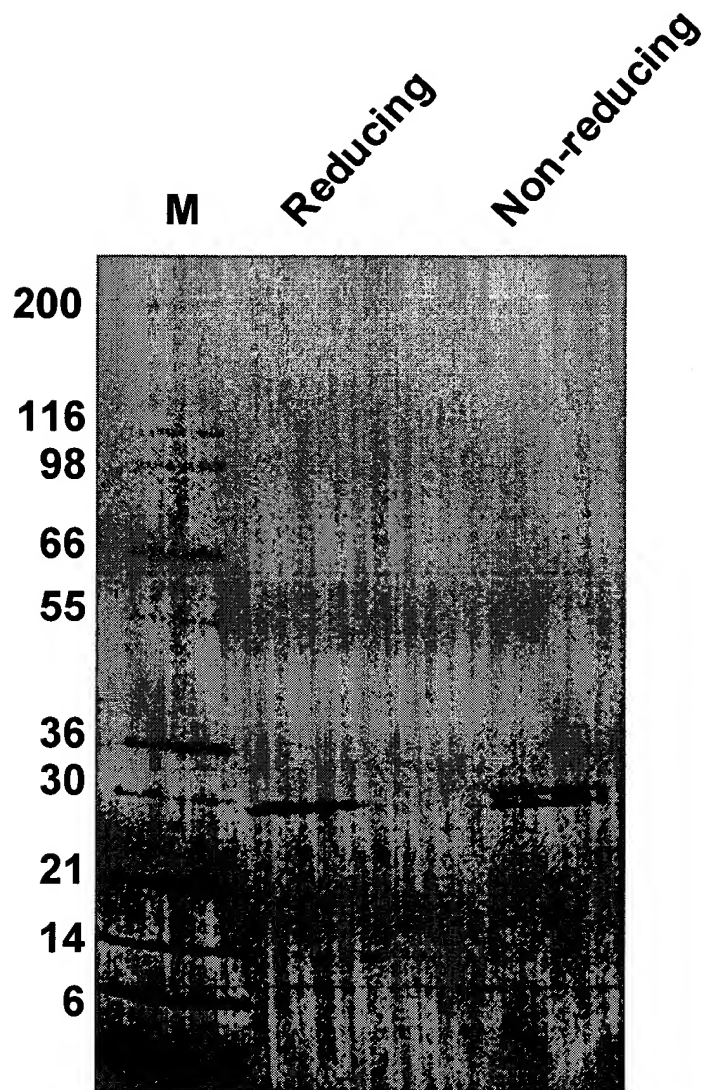
**Control**



**CG-AB020858**

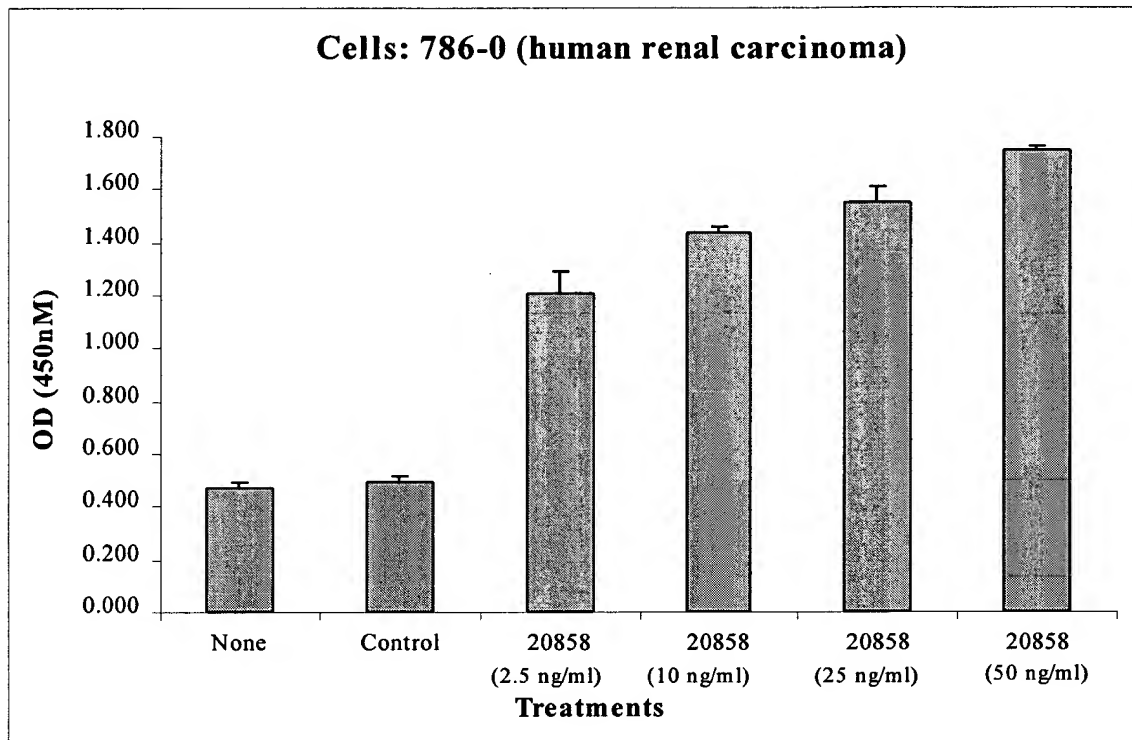


FIGURE 21.



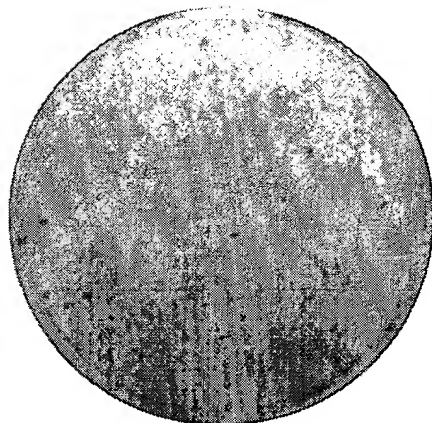


**FIGURE 22.**

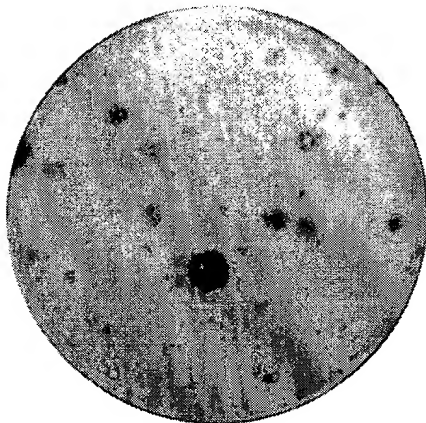


**FIGURE 23.**

Control



pFGF-20



pIgκ-FGF-20

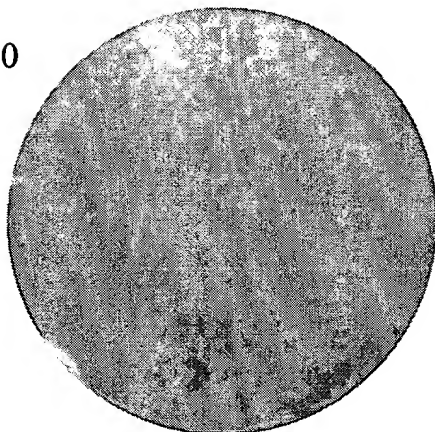


FIGURE 24

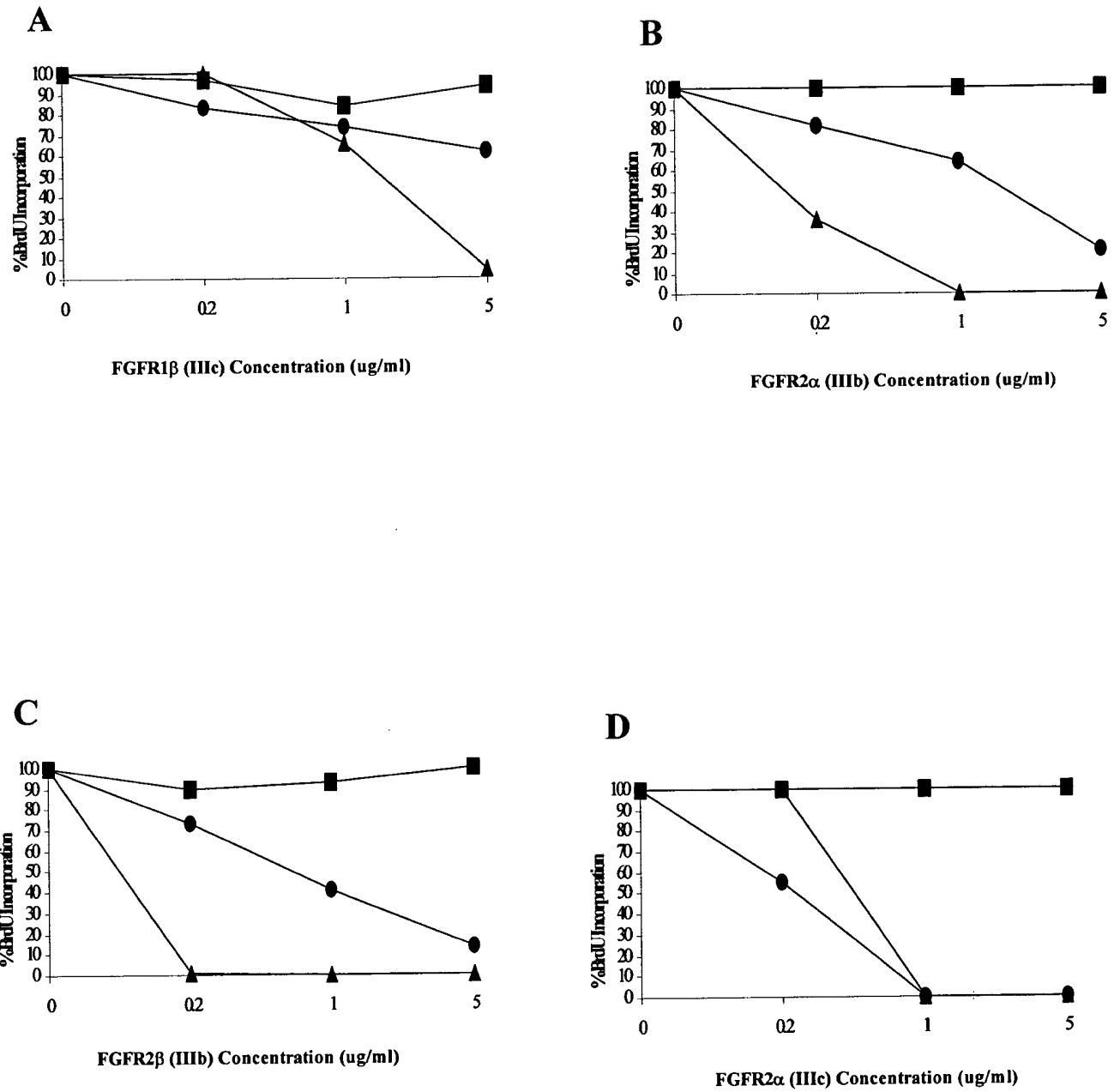


FIGURE 24 (ctd)

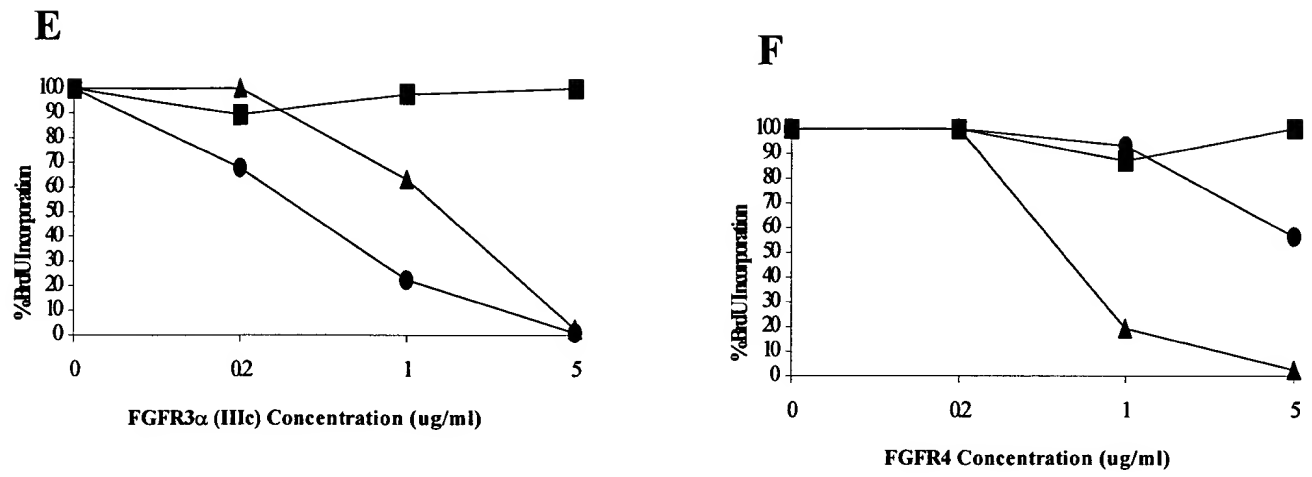


FIGURE 25

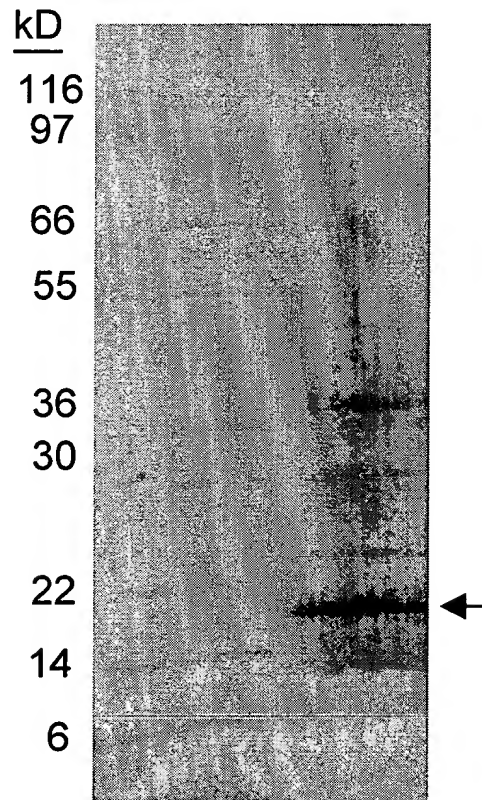


FIGURE 26

